



032301.202.seq.ST25.txt  
SEQUENCE LISTING

<110> BATHE, Brigitte

<120> NUCLEOTIDE SEQUENCES CODING FOR THE sigC GENE

<130> 032301 WD 202

<160> 4

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (300)..(878)

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taatcagccc ttacgtaaac tgccagcaaa aagacaaaag tatgatactt tttgcccact 240

ttgacacccc ctacacacct ttatggtgac cccggtctga actggtattc tgagcaatt 299

gtg aag tca aaa gag cgt aac gac gcc cac gtc acc gag ctg gcc cta 347

Met Lys Ser Lys Glu Arg Asn Asp Ala His Val Thr Glu Leu Ala Leu  
1 5 10 15

gcc gcc ggc cgt ggc gac cgc gca gct ctc acc gat ttc atc cgg gaa 395

Ala Ala Gly Arg Gly Asp Arg Ala Ala Leu Thr Asp Phe Ile Arg Glu  
20 25 30

acc caa gac gat gtc tgg cgt ctc ctc gcc cac ctt ggc ggc cac gaa 443

Thr Gln Asp Asp Val Trp Arg Leu Leu Ala His Leu Gly Gly His Glu  
35 40 45

atc gcc gac gat cta acc caa gaa act tat ctg cgg gtc atg agc gcc 491

Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu Arg Val Met Ser Ala  
50 55 60

ctc ccc cgc ttc gca gcg cgc tcc tcg gcg cgt acc tgg cta cta tcg 539

Leu Pro Arg Phe Ala Ala Arg Ser Ser Ala Arg Thr Trp Leu Leu Ser  
65 70 75 80

cta gcc cgg cgc gtc tgg gtc gac aac atc cga cac gac atg gca cgc 587

Leu Ala Arg Arg Val Trp Val Asp Asn Ile Arg His Asp Met Ala Arg  
85 90 95

ccc cgc aaa tcc atc gtc gaa tac gaa gac acc ggt gcc acc gac gcg 635

## 032301.202.seq.ST25.txt

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Pro Arg Lys Ser Ile Val Glu Tyr Glu Asp Thr Gly Ala Thr Asp Ala
100                               105                               110

agc aac gca ggc atc tgg tcc gag tgg atc gac gtg cgc acg ctt atc      683
Ser Asn Ala Gly Ile Trp Ser Glu Trp Ile Asp Val Arg Thr Leu Ile
115                               120                               125

gac gcc ctc cca ccc gaa cgc cgc gaa gcc ctc atc ctc acc caa gtg      731
Asp Ala Leu Pro Pro Glu Arg Arg Glu Ala Leu Ile Leu Thr Gln Val
130                               135                               140

ttg ggc tac acc tac gaa gaa gcc gca aaa atc gcc gac gtc cga gtc      779
Leu Gly Tyr Thr Tyr Glu Glu Ala Ala Lys Ile Ala Asp Val Arg Val
145                               150                               155                               160

gga aca atc cgt tcc cgc gta gcc cgc gcc aga gcg gac ctc att gct      827
Gly Thr Ile Arg Ser Arg Val Ala Arg Ala Arg Ala Asp Leu Ile Ala
165                               170                               175

gca aca gct acc ggt gat tcc tca gcc gaa gat ggc aaa tcc gcc caa      875
Ala Thr Ala Thr Gly Asp Ser Ser Ala Glu Asp Gly Lys Ser Ala Gln
180                               185                               190

ggc tagcagatga gctacgtcaa cggcgtaatc ccttaaccag attgctaatt      928
Gly

tacagttcta ttttgctgct cgatcaaagc gactcttacc caccctagaa tcctttgacc      988

gcacaaacac tttgttttta tctaaaactg aatctttaat ttttacgctc gcagatgatt    1048

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Thr Gln Asp Asp Val Trp Arg Leu Leu Ala His Leu Gly Gly His Glu
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Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu Arg Val Met Ser Ala
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Leu Pro Arg Phe Ala Ala Arg Ser Ser Ala Arg Thr Trp Leu Leu Ser  
65 70 75 80

Leu Ala Arg Arg Val Trp Val Asp Asn Ile Arg His Asp Met Ala Arg  
85 90 95

Pro Arg Lys Ser Ile Val Glu Tyr Glu Asp Thr Gly Ala Thr Asp Ala  
100 105 110

Ser Asn Ala Gly Ile Trp Ser Glu Trp Ile Asp Val Arg Thr Leu Ile  
115 120 125

Asp Ala Leu Pro Pro Glu Arg Arg Glu Ala Leu Ile Leu Thr Gln Val  
130 135 140

Leu Gly Tyr Thr Tyr Glu Glu Ala Ala Lys Ile Ala Asp Val Arg Val  
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Gly Thr Ile Arg Ser Arg Val Ala Arg Ala Arg Ala Asp Leu Ile Ala  
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Gly

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